

aggregation of arc-shaped protein assemblies leads to a cylindrical shape, although straight rods can also hold a membrane cylinder providing that its area is fixed (Figure 2A). Moreover, for Yop1p and Rtn1p proteins, the pathway of curvature creation is important. Fusion of small vesicles, stimulated by the presence in the membrane of Yop1p and Rtn1p, is likely to result in tubes rather than in spheres if the area to volume ratio is fixed, i.e. if the fusion is non-leaky [4,5]. Interestingly, fusion of the vesicles containing Yop1p or Rtn1p proceeds without specialized intracellular fusion proteins and is lipid insensitive [5]. The mechanism of the fusion reaction promoted by these proteins remains to be established.

The work of Hu *et al.* [5] shows that the DP1/Yop1p and reticulon family proteins represent a minimal protein machinery capable of creating an ER-like membrane morphology. Similar tubular networks can be created *in vitro* via microtubule-dependent membrane tethering by molecular motors [18]. However, Hu *et al.* [5] propose a plausible mechanism of curvature regulation that Yop1p arcs could implement in the formation of the ER tubules. Hopefully, many more illuminating studies will reveal how molecular motors and Yop1p arcs

synergistically orchestrate the morphology of the tubular ER and how the intracellular fusion machinery is involved in this curvature activity.

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## Batesian Mimicry: Can a Leopard Change Its Spots – and Get Them Back?

Can undefended mimics survive outside the range of their noxious models? Two recent studies on Batesian mimicry suggest they can, but alternative survival strategies and morphologies are then favoured.

Mathieu Joron

In 1862, in an influential paper which Darwin considered “one of the most remarkable and admirable papers [he] ever read in [his] life”, the British naturalist H.W. Bates described one of the most compelling examples of adaptation by natural selection [1]. In this paper Bates explained the extraordinary resemblance of unrelated butterflies in the Amazon

as adaptations by undefended species to fool insectivores into thinking they are of the unpalatable, forbidden kind. Mimicry has since been viewed as an illustration of the power of natural selection to shape traits and produce novel, adaptive morphologies. Examples such as Malayan octopus mimicking sea snakes, spiders mimicking ants, and day-flying, clearwing moths mimicking European wasps [2] are

particularly striking as the mimics have altered their shapes, colours and behaviours to resemble the typical morphologies of other classes or phyla.

Batesian mimicry is a parasitic relationship where mimics converge on an established warning signal used by noxious species (the ‘models’) and recognised by their predators. Predators avoid the patterns of the common defended species in their habitat, so the signal is stabilised by local density-dependent selection; the appearance of the warning signal itself is shaped to some extent by history and ecological contingency, and therefore varies deeply with geography [2]. Undefended mimics must ‘follow the fashion’ and vary in concert with their models, sometimes down to perplexing levels of details. Batesian mimicry is in effect an

epitome of local adaptation: mimics can only gain protection from mimicry if local predators have learned or evolved to avoid local models [2] (Figure 1).

The degree of mimetic resemblance is, however, much more variable than familiar examples suggest (Figure 1). Poor mimicry is common, for instance between some hoverflies and their wasp models, but the adaptive explanation for both indiscernible mimics and crude impressionistic copies is unclear [3,4]. What is needed is knowledge of the selection pressures and evolutionary histories that have produced different adaptive outcomes in different species or populations.

Two recent studies on classical examples of Batesian mimicry — noxious swallowtail butterflies [5] and coral snakes [6] — have investigated how the mimic responds to presence or absence of models. In each case, the palatable species spreads outside the geographical range of its model. This is surprising, because Batesian mimicry cannot, in theory, operate in the absence of models: brightly coloured mimics would soon attract the attention of predators that have not learned to avoid the model. Therefore, models usually maintain their warning signals across a wide range, while mimics tend to have more restricted ranges [2,7]. But these cases seem to bend the rules, allowing us to study the ecological and historical factors that shape mimetic adaptation.

Throughout the northern hemisphere, undefended admiral butterflies (genus *Limenitis*) have black wings with a white band. This is the case for the white admiral *L. arthemis* in northern North America, but southern US populations of this species (there known as the ‘red spotted purple’) have come to mimic the conspicuous bluish-black warning pattern of the toxic pipe vine swallowtail *Battus philenor*; the latter is also a model for multiple unrelated Batesian mimics including palatable female tiger swallowtails (*P. glaucus*) and day-flying male emperor moths. Other North American admirals have evolved mimicry of species with totally different wing patterns, most notably the viceroy *L. archippus* mimicking monarchs.

In one of the first studies of Batesian mimicry from a phylogenetic perspective, Prudic and Oliver [5] reconstructed gene genealogies of

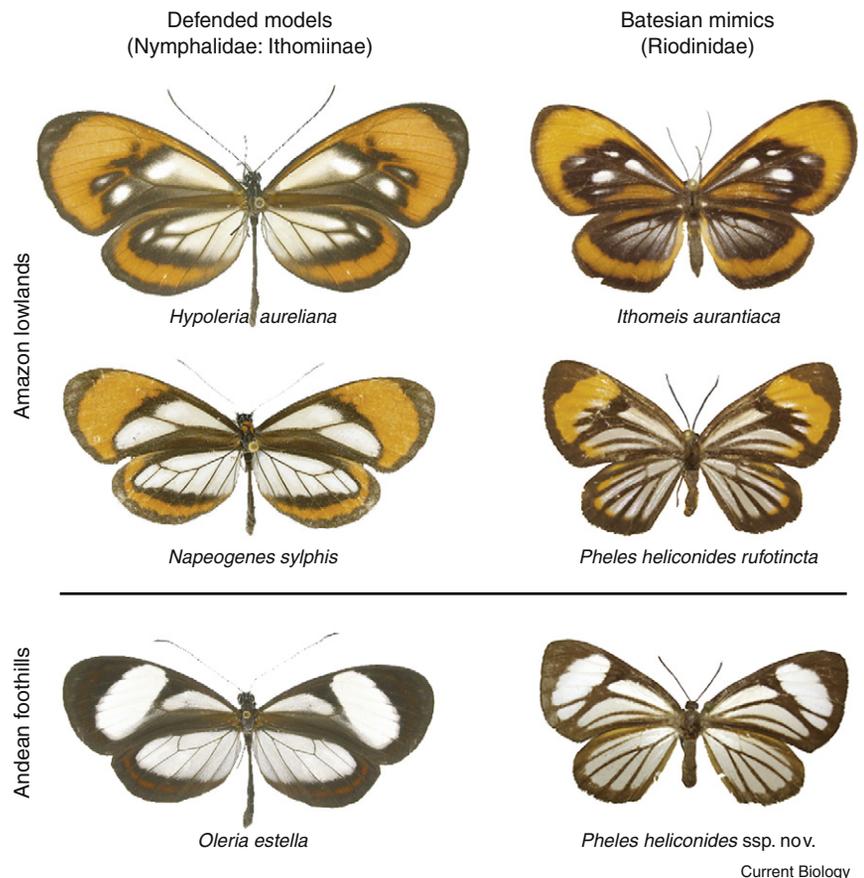


Figure 1. Batesian mimicry shifts across a faunal suture zone in Peru.

Mimicry represents a unique opportunity to study variation in the degree of local adaptation, since the warning signals used by local model species represent known fitness optima for mimics. Forest butterfly communities in Amazon are dominated by unpalatable clearwing butterflies (Nymphalidae: Ithomiinae, left) whose bodies contain pyrrolizidine alkaloids. In the lowlands of Eastern Peru, the orange-tip warning pattern is used by several species forming a mimicry ring (above line). But this warning pattern is abruptly replaced by a white-tip mimicry ring, as one moves into the Andean foothills (below line) [13]. Both patterns thus represent alternative fitness optima used in adjacent regions. Some metalmark butterflies (Riodinidae, right) are thought to be undefended Batesian mimics in these mimicry rings. Species that spread both in the lowlands and the foothills may change in concert with the models, such as the two *Pheles heliconides* races shown here, switching between adaptive peaks to adapt to locally common warning patterns. These mimetic shifts contrast with the shifts between mimicry and non-mimicry studied by Prudic and Oliver [5] and Harper and Pfennig [6] in North America. The distribution of mimicry in the Riodinidae suggests it evolved several times independently, and, as shown here, genera from unrelated tribes have come up with rather different ways of achieving mimicry, and have reached different degrees of mimetic resemblance.

*Limenitis* species and showed that Batesian mimicry has evolved three times from white-banded ancestors independently, once for monarch mimicry, once for mimicry of *Adelpha bredowii* and once for swallowtail mimicry. Within the *L. arthemis* species, however, individuals from non-mimetic (northern) populations are nested within a clade of swallowtail mimics. Prudic and Oliver [5] thus infer that, in areas without the noxious model, selection against conspicuous bluish-black patterns led the mimic to revert to the

ancestral admiral wing pattern, thought to be less visible through disruptive coloration [8]. Wing patterns representing alternative strategies of protection can therefore be selected in different areas of the range, independently of the genealogy of populations.

A comparable situation is found in the harmless kingsnake *Lampropeltis triangulum*. Although a clear mimic of deadly coral snakes (*Micrurus fulvius*) in southern parts of North America, the scarlet kingsnake (*L. t. elapsoides*) extends north into an area of several

hundred square kilometres where no coral snakes are found. Harper and Pfennig [6] quantified the variation of the mimic's patterns and showed that resemblance to coral snakes decreases gradually as one moves away from the zone of sympatry with models. Furthermore, this is mirrored by an increase in predator attacks on good relative to poor mimetic patterns, which the authors measured using painted plasticine dummy snakes placed in the wild. As expected from theory, the advantages of mimicry in sympatry become disadvantages in the absence of models, in which case patterns with less black banding are favoured. But the mimic's pattern does not revert to an ancestral kingsnake pattern; instead, it shifts towards a more reddish pattern that is probably better camouflaged in the deciduous forests of areas of allopatry, as well as during low-light hours (G.R. Harper and D.W. Pfennig, personal communication).

Both new studies [5,6] thus show that mimetic species are not necessarily constrained by their model's range, but can expand away from their model where alternatives to mimetic patterns are favoured. The extent of mimicry seems to follow the outcome of a balance between selection for and against mimicry around the boundary of sympatry with models.

So, if crypsis is an effective anti-attack alternative to mimicry, is the mimicry frontier situated just where the benefits of mimicry in sympatry offset the costs of conspicuousness in allopatry? If that were the case, a gradual cline of resemblance should be centred on the boundary of sympatry through classic migration-selection balance. The study of kingsnakes suggests something quite different: an earlier study showed that the best mimics were found near the edge of the area of sympatry, where coral snakes are least abundant [4]; mimicry then breaks down gradually in allopatry [6]. The shape of mimicry decline thus suggests selection for mimicry is far stronger than selection against conspicuousness, even where models are scarce [4,6].

One reason why mimicry appears to prevail against the baseline strategy of protection through hiding might lie in additional advantages brought by mimetic protection. Mimicry allows

individuals to utilise their habitat more efficiently: foraging, basking, and other activities can be performed in full visibility and at lower body temperatures, bearing neither the energetic cost of alertness and escape, nor the constraints of remaining hidden or camouflaged [2,9]. Opportunity and physiological benefits might generally put more weight on the mimicry side of the balance at the boundary of the model's distribution, or, likewise, in the early stages of mimicry evolution.

It is striking, however, that the breakdown of mimicry in snakes is gradual and incomplete. Because coral snakes are deadly dangerous, predators have evolved an innate aversion of their patterns, which may spread outside the snakes' range through dispersal, and may respond slowly to changes in coral snake density. In contrast, unpalatable butterflies are less dangerous, so the diet composition of insectivores is largely based on learning and repeated experimentation [10,11]. This might explain the contrast between the slow erosion of snake mimicry over hundreds of kilometres, versus the sharp, 'fashion-like' spatial and temporal adjustments known in butterfly mimicry [1,12,13].

One crucial unknown factor is, however, the genetic basis of mimicry breakdown in allopatry. Neutral molecular markers reveal the phylogeographic history underlying the current distribution of populations, and therefore the directionality of mimetic change at the broad scale: *Limenitis* admirals colonised North America from the northeast before reaching the range of distasteful *Battus* swallowtails [14], while kingsnakes have originated in sympatry with their coral snake models [6]. Unfortunately, phylogenies in recent lineages fall short of revealing the history of adaptation itself, because the genealogies of genes under strong selection may be very different. Here, one of the challenges clearly lies in understanding the genetic history of the actual adaptive alleles [15,16]. Melanism in mimetic butterflies and in reptiles commonly involves mutations just at a few loci of large effect [17,18]. Such flexible control may, indeed, easily revert to cryptic phenotypes — in fact, many butterfly Batesian mimics retain cryptic undersides, and in some species mimetic and non-mimetic forms coexist in sympatry [2]. However, strong selection also allows mimicry

alleles to spread like wildfire through populations and continents, independently of much of the genome [12,19,20]. Thus, mimicry may well have appeared in just one lineage and rapidly spread to other lineages, in discordance with the genealogy of other genes. With the availability of new genetic tools for marker development and gene discovery, the patterns of geographical variation in both snake and butterfly mimicry represent fantastic opportunities to study the spread of different adaptive strategies at the molecular level.

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## Cytokinesis: Keeping Ring and Membrane Together

During cytokinesis, the actomyosin contractile ring drives ingression of the overlying plasma membrane. A recent study has provided mechanistic insight into how the contractile ring might contribute to membrane ingression.

Manuel Mendoza and Yves Barral

Cytokinesis, the division of one cell into two, initiates towards the end of mitosis, when the plasma membrane invaginates between the segregating chromosomes [1–3]. The region of the membrane undergoing this deformation, known as the cleavage furrow, is tightly associated with the contractile ring, a sub-cortical meshwork of actin and myosin filaments. In most animal cells, furrow ingression depends on actomyosin ring contraction, and extensive analysis of ring components has shed light on the mechanism of ring assembly and contraction (for reviews, see [1–4]). Surprisingly, however, we know very little about how ring dynamics are coupled to changes in membrane shape during cytokinesis. For example, how does the ring associate with the membrane? What is the relationship between ring-generated forces and membrane deformation? New insights into these questions have been provided by the recent identification of a budding yeast protein that couples membrane ingression to ring contraction [5].

Since the discovery 12 years ago that budding yeast, like animal cells, assemble an actomyosin contractile ring during cytokinesis [6,7], it is now accepted that yeast and animal cell-division machineries have many similarities. In the recent work, Sanchez-Diaz and co-workers [5] identified *Inn1* (*ingression 1*), a novel component of the yeast contractile ring required for cytokinesis. Analysis of *Inn1*-depleted cells revealed a striking phenotype: unlike any other

cytokinesis mutant known so far, inactivation of *Inn1* causes the actomyosin ring to detach from the plasma membrane upon contraction. Rings lacking *Inn1* undergo normal contraction, but the membrane fails to invaginate. *Inn1* therefore plays a crucial role in the coupling of membrane ingression and actomyosin contractility.

So, how does *Inn1* couple ingression of the plasma membrane to actomyosin ring contraction? The amino-terminal region of *Inn1* is predicted to form a C2 domain, a protein fold known to bind biological membranes [8]. The remainder of the protein is rich in PXXP motifs, which are often sites of protein–protein interactions. The study by Sanchez-Diaz *et al.* [5] suggests that *Inn1* physically links the membrane and the contractile ring, with its C2 domain binding to the plasma membrane and the rest of the protein anchoring *Inn1* to the ring (Figure 1), a model supported by various findings. Localization of *Inn1* to the site of cell division depends on ring assembly, and the protein physically interacts with the ring components Hof1 and Iqg1.

Furthermore, deletion of the C2 domain, or point mutations that disrupt C2-domain-dependent interactions, do not abolish the localization of *Inn1* mutant proteins to the cleavage site, but impair cytokinesis. It is therefore likely that *Inn1* localizes to the division site through direct association with the ring and that the C2 domain is required for association with the membrane. To directly assess whether *Inn1* couples membrane deformation to actin-ring contraction through its C2 domain,

the authors targeted the C2 domain to the furrow by fusing it to the ring component Hof1. This C2–Hof1 fusion protein completely rescued cytokinesis in *inn1Δ* cells. Similar results were obtained by fusing the C2 domain of *Inn1* to Myo1, the yeast myosin II motor. *Inn1* therefore couples ring contraction and membrane ingression, apparently by directly linking the ring with the plasma membrane.

Does *Inn1* act as ‘molecular velcro’ attaching the plasma membrane to the contractile ring? The reality seems to be more complicated. Correct positioning, assembly and contractility of the ring do not require *Inn1*, which is incorporated in the ring shortly before contraction. Thus, the initial association between ring and membrane must depend on factors other than *Inn1*. Indeed, multiple lipid-binding proteins associate with the division site [9] and could contribute to this initial membrane attachment. So why is *Inn1* essential

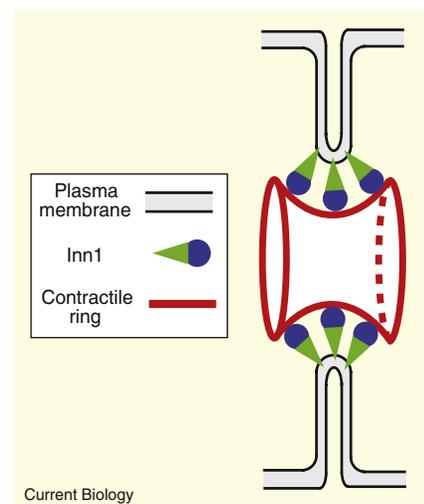


Figure 1. Schematic representation of how *Inn1* couples actomyosin ring contraction to membrane ingression during cytokinesis. *Inn1* associates with the plasma membrane through its amino-terminal C2 domain (represented in green) whereas its carboxy-terminal portion (in blue) binds the contractile ring.